Polyadenylation of SARS-CoV-1 genomic RNA (plus strand)

Acencio, ML., Mazein, A., Orlic-Milacic, M.
Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references


Reactome database release: 77

This document contains 1 reaction (see Table of Contents)
Polyadenylation of SARS-CoV-1 genomic RNA (plus strand)

Stable identifier: R-HSA-9685519

Type: uncertain

Compartments: cytosol

Diseases: severe acute respiratory syndrome

SARS-CoV-1 plus strand genomic RNA, like genomic RNAs of other coronaviruses, possesses a polyadenylation signal in its 3'UTR and is polyadenylated by an undetermined viral RNA polymerase, possibly nsp8 or nsp12 (Spagnolo and Hogue 2000, Peng et al. 2016, Tvarogova et al. 2019).

Literature references


Editions

<table>
<thead>
<tr>
<th>Date</th>
<th>Action</th>
<th>Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>2020-04-30</td>
<td>Authored</td>
<td>Orlic-Milacic, M.</td>
</tr>
<tr>
<td>2020-05-11</td>
<td>Edited</td>
<td>Orlic-Milacic, M.</td>
</tr>
<tr>
<td>2020-05-27</td>
<td>Reviewed</td>
<td>Mazein, A., Acencio, ML.</td>
</tr>
</tbody>
</table>